class05.R

Andres

2021-10-13

```r
#Class 5: Data Visualization

library(ggplot2)
ggplot(cars)
```



```r
head(cars)
```
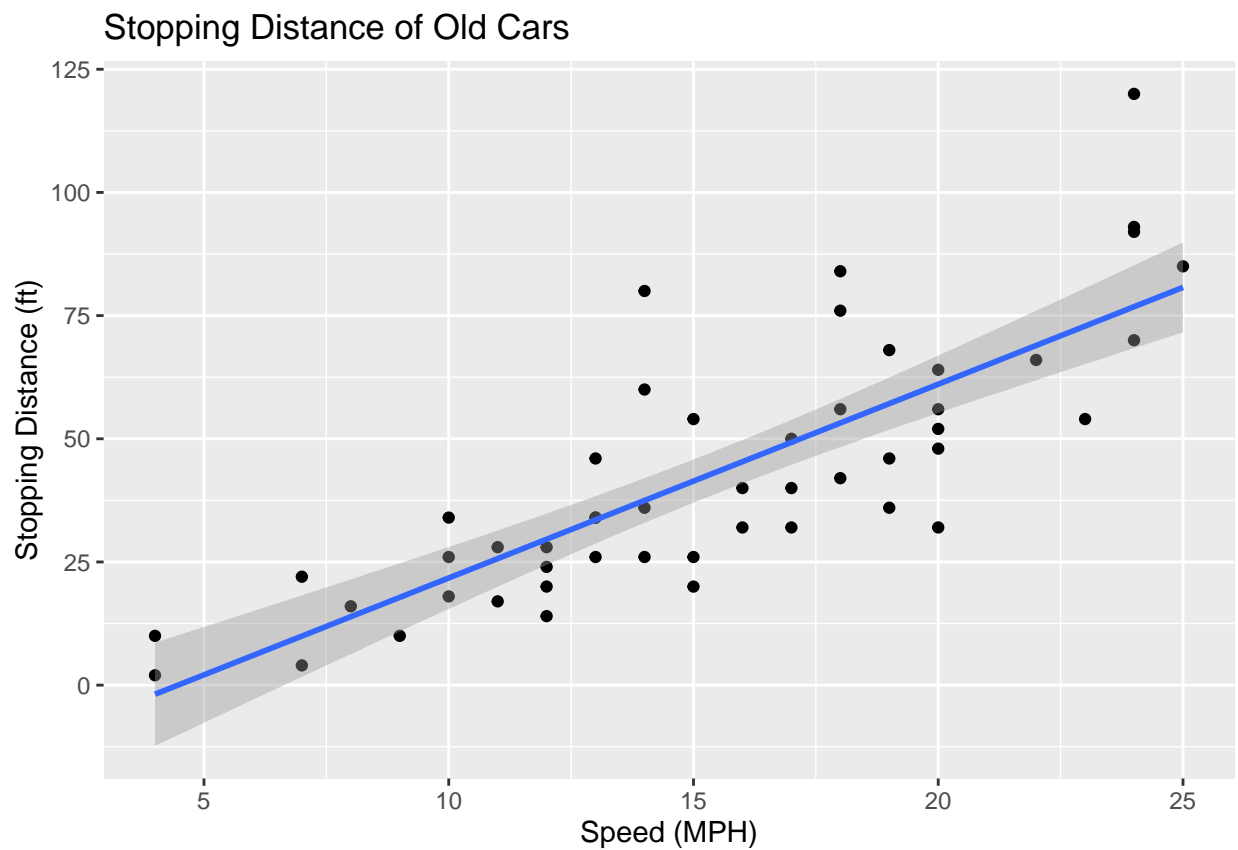
```
##   speed dist
## 1     4    2
## 2     4   10
## 3     7    4
## 4     7   22
## 5     8   16
## 6     9   10
```

```
tail(cars)
```
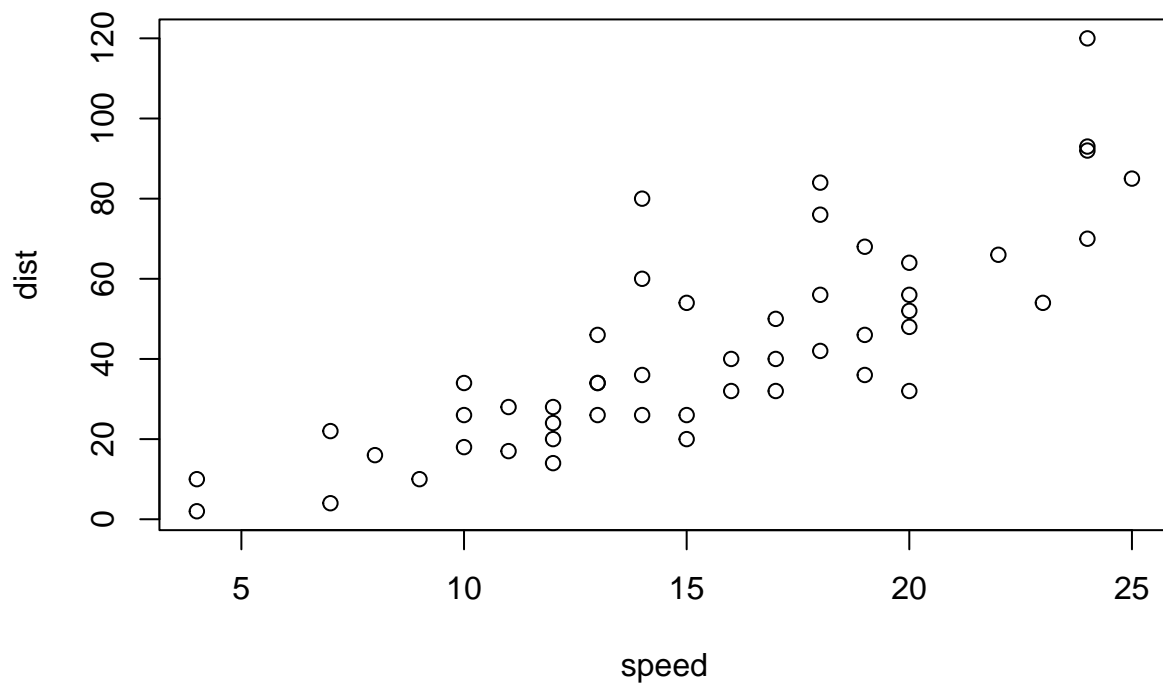
```
##    speed dist
## 45    23   54
## 46    24   70
## 47    24   92
## 48    24   93
## 49    24  120
## 50    25   85
```

```
ggplot(data=cars)+aes(x=speed, y=dist)+
  geom_point()+
  geom_smooth(method="lm")+
  labs(title="Stopping Distance of Old Cars",
       x="Speed (MPH)",
       y="Stopping Distance (ft)")
```

```
## `geom_smooth()` using formula 'y ~ x'
```



```
# ggplot is not the only graphic system. Another is "base"
plot(cars)
```

```
url <- "https://bioboot.github.io/bimm143_S20/class-material/up_down_expression.txt"
genes <- read.delim(url)
head(genes)
```

```
##          Gene Condition1 Condition2      State
## 1       A4GNT -3.6808610 -3.4401355 unchanging
## 2        AAAS  4.5479580  4.3864126 unchanging
## 3       AASDH  3.7190695  3.4787276 unchanging
## 4        AATF  5.0784720  5.0151916 unchanging
## 5        AATK  0.4711421  0.5598642 unchanging
## 6  AB015752.4 -3.6808610 -3.5921390 unchanging
```

```
tail(genes)
```

```
##          Gene Condition1 Condition2      State
## 5191  ZSCAN23  0.1715818  0.1448267 unchanging
## 5192  ZSCAN30  3.8720214  4.1523213 unchanging
## 5193     ZW10  5.3989200  5.2251997 unchanging
## 5194     ZXDA  3.2784970  3.3800430 unchanging
## 5195   ZYG11B  6.1400270  6.1086860 unchanging
## 5196      ZYX  4.1221940  4.1597770 unchanging
```

```
nrow(genes)
```

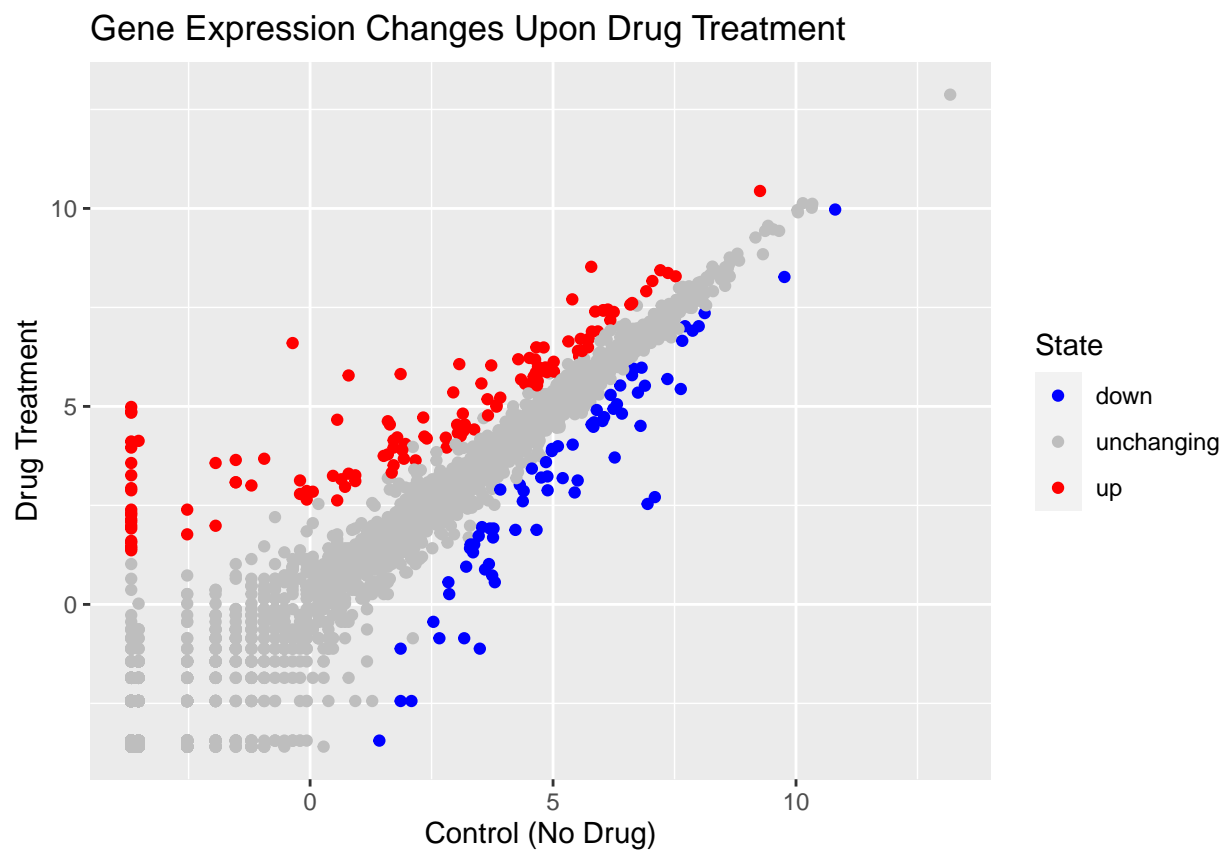```
[1] 5196
```

```
colnames(genes)
```

```
## [1] "Gene"       "Condition1" "Condition2" "State"
```

```
round(table(genes$State)/nrow(genes)*100,2)
```

```
##
##       down unchanging          up
##       1.39      96.17        2.44
```

```
p <- ggplot(genes)+aes(x=Condition1, y=Condition2, col=State)+ geom_point()
q <- p + scale_colour_manual(values=c("blue", "gray","red"))+
  labs(title = "Gene Expression Changes Upon Drug Treatment",
       x="Control (No Drug)", y="Drug Treatment")
#First graph of the lab
q
```



```
#SECOND EXERCISE
```

```
library(gapminder)
```

```
library(dplyr)
```
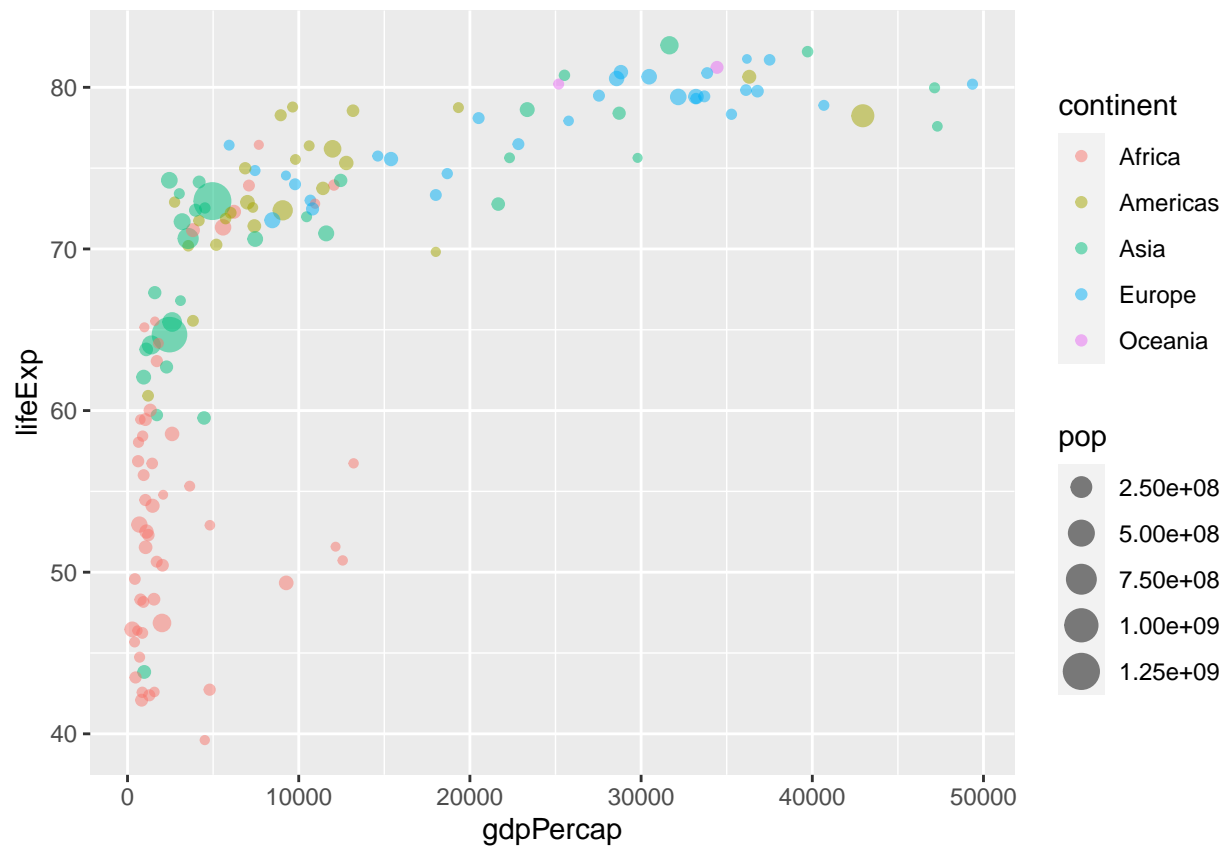
```
##
## Attaching package: 'dplyr'


## The following objects are masked from 'package:stats':
##
##     filter, lag


## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```
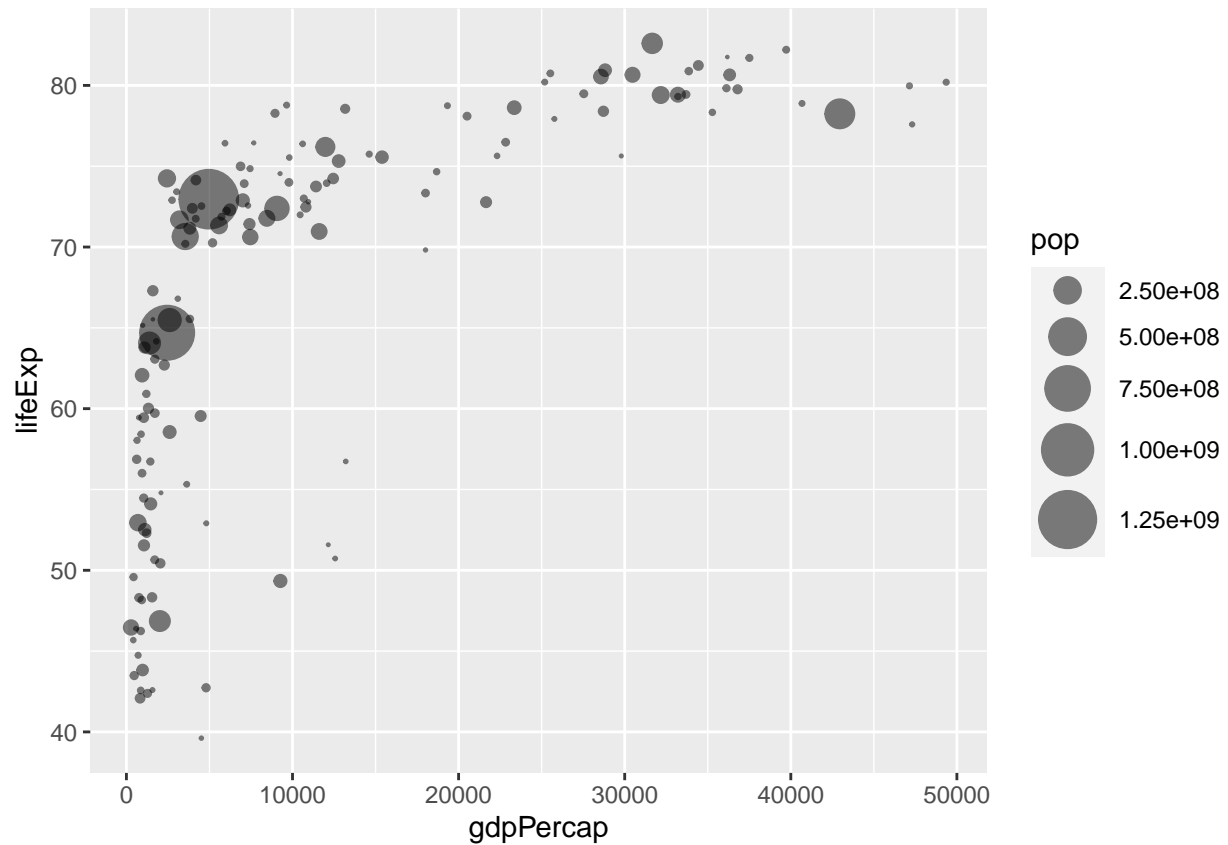
```r
gapminder_2007 <- gapminder %>% filter(year==2007)

ggplot(gapminder_2007) +
  aes(x=gdpPercap, y=lifeExp, color=continent, size=pop) +
  geom_point(alpha=0.5)
```
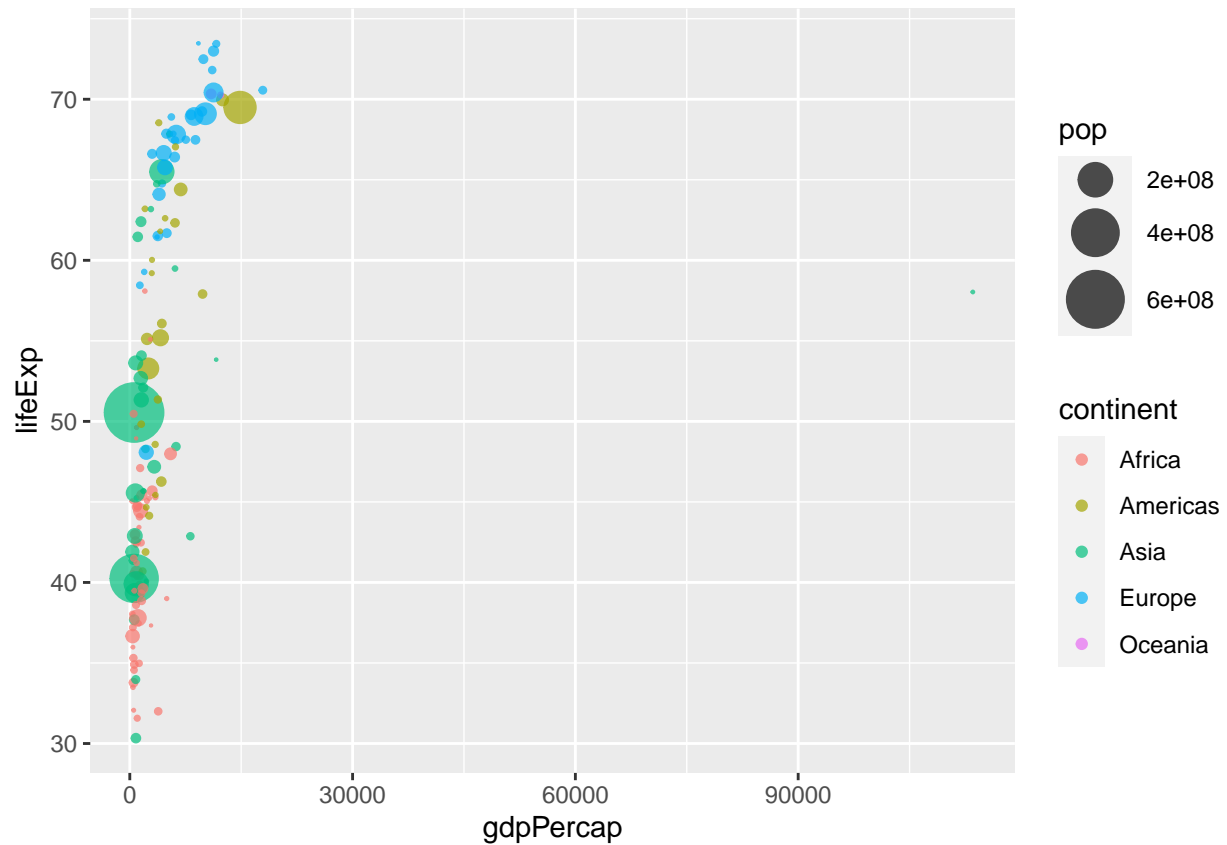


```r
#Graph for 2007

ggplot(gapminder_2007) +
  geom_point(aes(x=gdpPercap, y=lifeExp, size=pop), alpha=0.5) +
  scale_size_area(max_size = 10)
```

```
r <- ggplot(gapminder_2007) +
  geom_point(aes(x=gdpPercap, y=lifeExp, size=pop), alpha=0.5) +
  scale_size_area(max_size = 10)
gapminder_1957 <- gapminder %>% filter(year==1957)
#Graph for 1957
ggplot(gapminder_1957) +
  aes(x = gdpPercap, y = lifeExp, color=continent,size = pop) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size = 10)
```

```
t <-ggplot(gapminder_1957) +
  aes(x = gdpPercap, y = lifeExp, color=continent,size = pop) +
  geom_point(alpha=0.7) +
  scale_size_area(max_size = 10)

gapminder_1957and2007 <- gapminder %>% filter(year==1957 | year==2007)
#Comparison of 1957 and 2007
ggplot(gapminder_1957and2007) +
  geom_point(aes(x = gdpPercap, y = lifeExp, color=continent,size = pop), alpha=0.7) +
  scale_size_area(max_size = 10) + facet_wrap(~year)
```
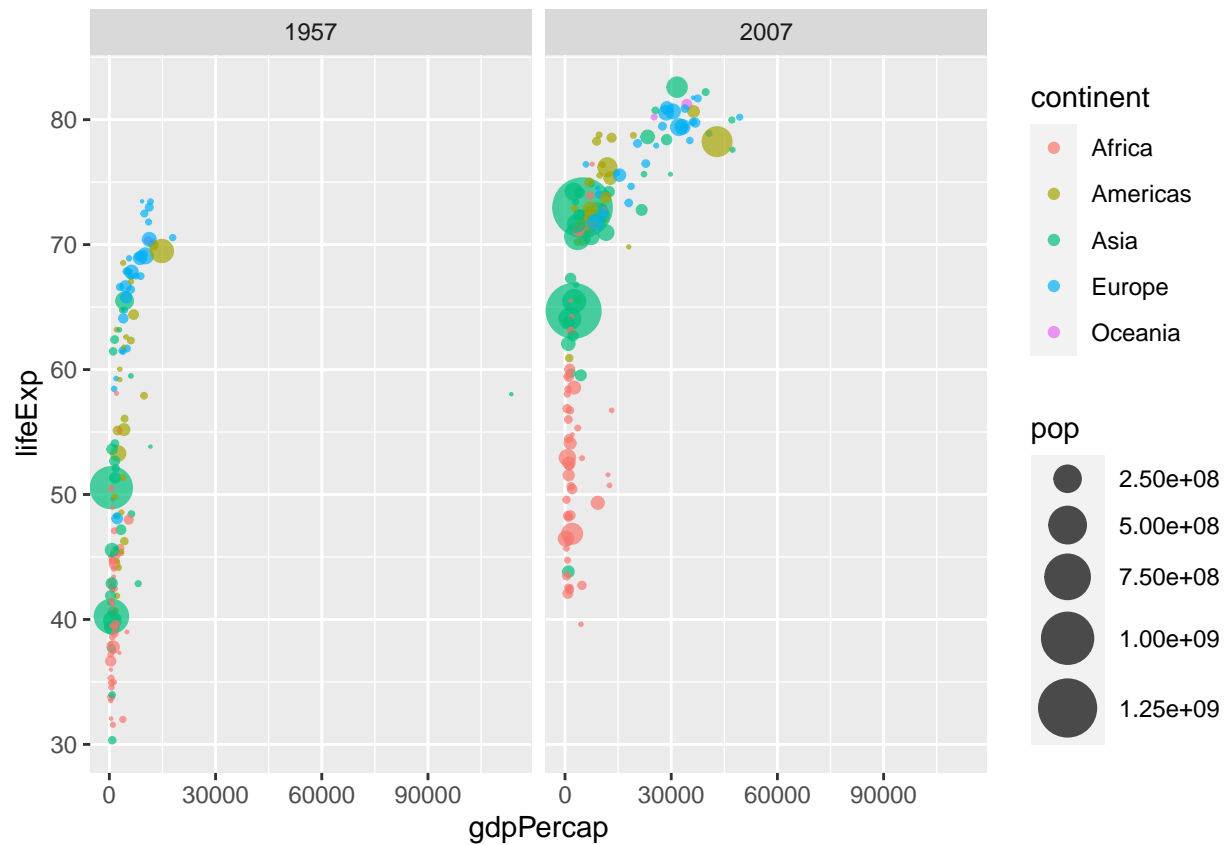
```
ggplot(gapminder) + aes(x=year, y=lifeExp, col=continent)+geom_jitter(width=0.3,alpha=0.4)+
   geom_violin(aes(group=year), alpha=0.2, draw_quantiles = 0.5)
```
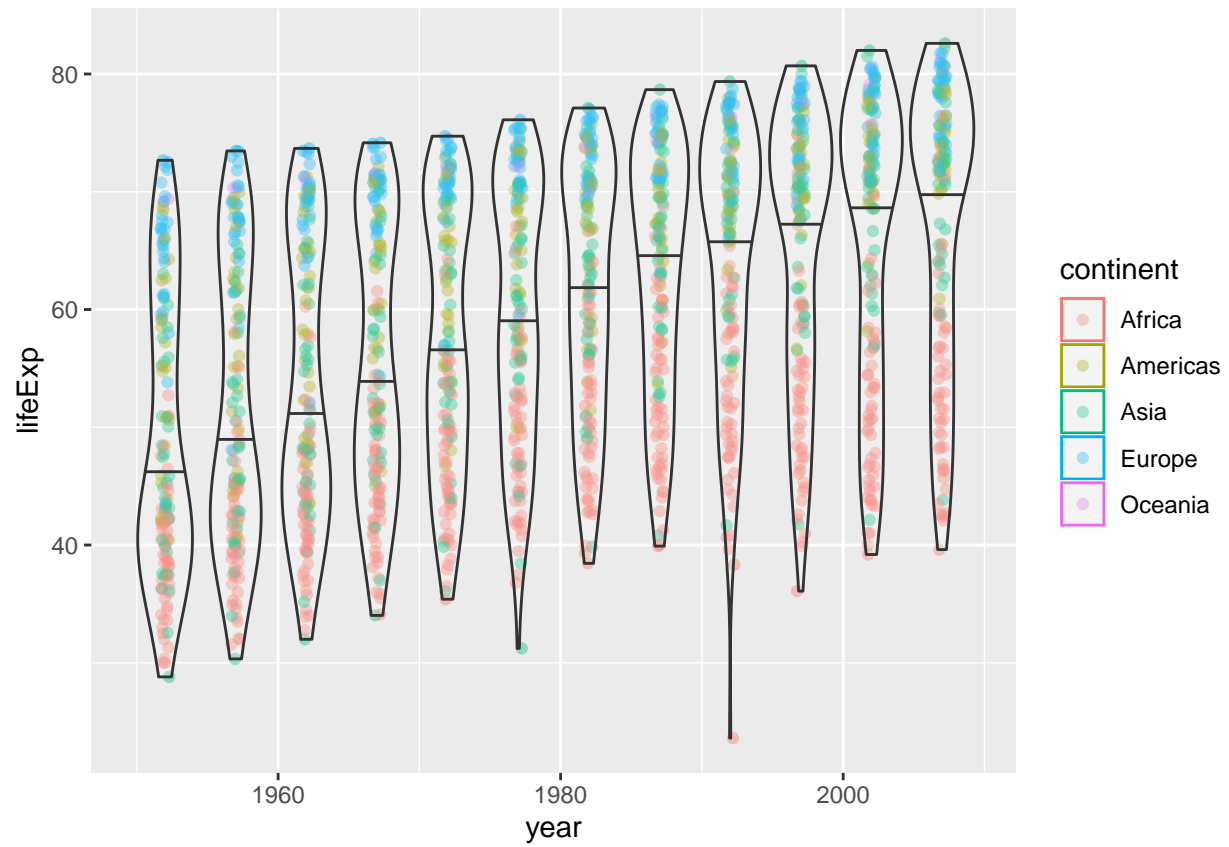
```
#Install the plotly
#library(plotly)
#ggplotly()
```